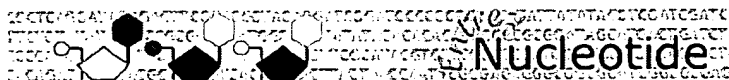


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481 tcgcacccta ncatccttaa aacgcacngc tccgcctga
```

```
//
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Revised: October 24, 2001.

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[NCBI](#) | [NLM](#) | [NIH](#)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books
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Limits		Preview/Index		History		Clipboard		Details
Display	<input type="text" value="GenBank"/>	Save	Text	Add to Clipboard				

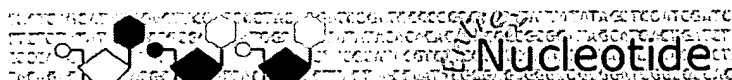
☐ 1: W91831. est_A V cDNA sub...[gi:1663765]

PubMed, Taxonomy, LinkOut

LOCUS W91831 118 bp mRNA EST 10-AUG-1998
 DEFINITION est_A V cDNA subtractive library Drosophila melanogaster cDNA clone B3, mRNA sequence.
 ACCESSION W91831
 VERSION W91831.1 GI:1663765
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 118)
 AUTHORS Casal, J. and Leptin, M.
 TITLE Identification of novel genes in Drosophila reveals the complex regulation of early gene activity in the mesoderm
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93, 10327-10332 (1996)
 MEDLINE 96413645
 COMMENT Contact: Casal J (UK) or Leptin M (D)
 Laboratory of Molecular Biology (UK) or Institut fuer Genetik (D)
 Medical Research Council (UK) or Universitaet zu Koeln (D)
 Hills Road, Cambridge CB2 2QH, England, or, Weyertal 121, D-50931 Koeln, Germany
 Tel: (1223)402282 (UK) or (221)4703401 (D)
 Fax: (1223)412142 (UK) or (221)4705264 (D)
 Email: jecl@mrc-lmb.cam.ac.uk (UK) or mleptin@genetik.uni-koeln.de (D).
 FEATURES
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 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="B3"
 /clone_lib="V cDNA subtractive library"
 /note="Vector: pBluescript II; cDNA library from T1[10b] embryos minus cDNAs from T1[r444]/T1[9QRX] embryos"
 BASE COUNT 38 a 13 c 19 g 41 t 7 others
 ORIGIN
 1 tgcttngaga gtaactttat ttnctccac tagaaatttt acaatgaaat atttgaaat
 61 ncgattacgt ttatagttag tnttaagt tagtaggaaa atnaattgcaaatngcct
 //

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	Books
Search <input type="text" value="Nucleotide"/> for <input type="text"/>							Go	Clear
Limits		Preview/Index		History		Clipboard		Details
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☐ 1: AA140991. CK01064.3prime CK...[gi:1704453]

Taxonomy

LOCUS AA140991 520 bp mRNA EST 29-NOV-1998
 DEFINITION CK01064.3prime CK Drosophila melanogaster embryo BlueScript
 Drosophila melanogaster cDNA clone CK01064 3prime, mRNA sequence.
 ACCESSION AA140991
 VERSION AA140991.1 GI:1704453
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM *Drosophila melanogaster*
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; *Drosophila*.
 REFERENCE 1 (bases 1 to 520)
 AUTHORS Kopczynski,C., Serano,T., Rubin,G. and Goodman,C.
 TITLE BDGP/HHMI CK Drosophila EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Insert Length: 520 Std Error: 0.00
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 High quality sequence stop: 520.
 FEATURES
 source Location/Qualifiers
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 /clone="CK01064"
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 /sex="male and female"
 /dev_stage="0 to 24 hours old embryo"
 /lab_host="XL1 Blue MRF"
 /note="Organ: embryo; Vector: Bluescript SK; Site_1: ClaI;
 Site_2: PstI; mRNA purified from rough endoplasmic
 reticulum-bound polysomes was used as a template. cDNA's
 directionally cloned at HindIII and PstI in Bluescript
 SKt. Cloned into HindIII, but the site was destroyed to
 add an adapter sequence. So ClaI is now the restriction
 enzyme at site I of vector. Primers - 5' universal, 3'
 ml3-20 (reverse), 3' T3, 5' T7."
 BASE COUNT 98 a 140 c 113 g 163 t 6 others
 ORIGIN
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 61 tatttggaaa tacgattacg tttatagtta ggggttaagt gtagtaggaa aatgaattgc
 121 aaatagcctg ccggtcgtcg ggtgttttcc ccgtgccgcc acacaaaatc tcagccatgt
 181 cgtgttcacg tggacttggt tttttgggat ctggtttctg gtttntattt gttttgtttt
 241 gccatcctgg tcatcaggcg cagtagtcca gtatatcgtc gtaggtgcag ccctccttgc
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 361 ggtggcacac cccttctccg ttatccgcgt ccgtttgcct tcctgcttta aaccttcccc